

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,109

DATE: 05/29/2001
TIME: 15:37:28

Input Set : A:\SeqListing.APP.txt
Output Set: C:\CRF3\05292001\I674109.raw

3 <110> APPLICANT: HOECHST MARION ROUSSEL
5 <120> TITLE OF INVENTION: METHOD FOR SCREENING ANTIMYCOTIC SUBSTANCES USING
6 ESSENTIAL GENES FROM S.CEREVIRIAE
8 <130> FILE REFERENCE: 16363PC RUU 7
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/674,109
C--> 11 <141> CURRENT FILING DATE: 2000-11-22
13 <150> PRIOR APPLICATION NUMBER: 98402254.1
14 <151> PRIOR FILING DATE: 1998-09-11
16 <150> PRIOR APPLICATION NUMBER: 98401007.4
17 <151> PRIOR FILING DATE: 1998-04-24
E--> 19 <160> NUMBER OF SEQ ID NOS: 180
21 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

1337 <210> SEQ ID NO: 106 Seq #106, number of bases differ:
1338 <211> LENGTH: 62 - 62 listed
1339 <212> TYPE: DNA - 54 shown
1340 <213> ORGANISM: Artificial Sequence
1342 <220> FEATURE:
1343 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
1344 YML049c-S1
1346 <400> SEQUENCE: 106
E--> 1347 aattcctgct cattcaagga aagtctcagg aaattttcac cagctgaagc ttcgtacgc 59
1474 <210> SEQ ID NO: 117 Seq #117, number of bases differ:
1475 <211> LENGTH: 59 - 54 listed
1476 <212> TYPE: DNA - 62 shown
1477 <213> ORGANISM: Artificial Sequence
1479 <220> FEATURE:
1480 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
1481 YMR211w-S2
1483 <400> SEQUENCE: 117
1484 atttcaatca tcttactccg tgaatcaggt tcggaatgtat gcataggcca ctatggatc 60
E--> 1485 tg 62
2265 <210> SEQ ID NO: 180
2266 <211> LENGTH: 62
2267 <212> TYPE: DNA
2268 <213> ORGANISM: Artificial Sequence
2270 <220> FEATURE:
2271 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
2272 YPR137w-S2
2274 <400> SEQUENCE: 180
2275 aaaagcctgt ttgtcaatg acagctgaat atataccatt gcataggcca ctatggatc 60
2276 tg 62
W--> 2279 imer
E--> 2280 ymr290c-s1 Seq # 3

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Input Set : A:\SeqListing.APP.txt
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W--> 2282 <210> SEQ ID NO:
W--> 2282 <211> LENGTH:
W--> 2282 <212> TYPE:
W--> 2282 <213> ORGANISM:
E--> 2282 <400> SEQUENCE: 105
2283 tgagtttac gtcttttgtt atttggcggtt tttccactgg cagctgaagc ttcgtacgc 59
2285 <210> SEQ ID NO: 106
2286 <211> LENGTH: 68
2287 <212> TYPE: DNA
2288 <213> ORGANISM: Artificial Sequence
2290 <220> FEATURE:
2291 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
2292 YML049c-S1
2294 <400> SEQUENCE: 106
E--> 2295 aattcctgct cattcaagga aagtctcagg aaatttcac cagctgaagc ttcgtacgc 59
2422 <210> SEQ ID NO: 117
2423 <211> LENGTH: 59
2424 <212> TYPE: DNA
2425 <213> ORGANISM: Artificial Sequence
2427 <220> FEATURE:
2428 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
2429 YMR211w-S2
2431 <400> SEQUENCE: 117
2432 aattcaatca tcttactccg tgaatcaggt tcggaatgtat gcataggcca ctatggatc 60
E--> 2433 tg

↑
Disregard, these are errors due
to the duplication of sequences 105-
to 153 as shown on p. 3.

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P 3

<210> 180 → Seq. 180 - listed as last on the file.
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
YPR137w-S2

<400> 180
aaaaggcctgt ttggtaatg acagctgaat atataccatt gcataggcca ctagtggatc 60
tg

~~delete~~ ^{more} ~~YMR290c-S1~~ → After sequence 180, the listing starts
over at sequence # 105 and goes to
sequence # 153. All of this duplication
must be deleted from the file.

<400> 105
tggatttac gtcttttgtt atttggcggtt tttccactgg cagctgaagc ttcgtacgc 59

<210> 106
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
YML049c-S1

<400> 106
aattcctgct cattcaagga aagtctcagg aaattttcac cagctgaagc ttcgtacgc 59

<210> 107
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
YMR290c-S2

<400> 107

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/674,109

DATE: 05/29/2001

TIME: 15:37:30

Input Set : A:\SeqListing.APP.txt
Output Set: C:\CRF3\05292001\I674109.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1347 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:59 SEQ:106
L:1485 M:252 E: No. of Seq. differs, <211>LENGTH:Input:59 Found:62 SEQ:117
L:2279 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:180
L:2280 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:68 SEQ:180
L:2280 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:2280 M:112 C: (48) String data converted to lower case,
L:2280 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:68 SEQ:180
L:2282 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:2282 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:2282 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:2282 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:2282 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:180 differs:105
L:2295 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:59 SEQ:106
L:2433 M:252 E: No. of Seq. differs, <211>LENGTH:Input:59 Found:62 SEQ:117
L:19 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (180) Counted (228)